

1 / 8

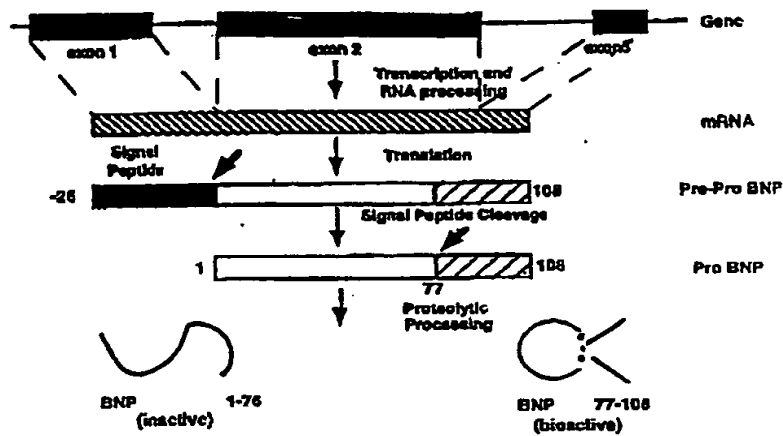


Fig 1

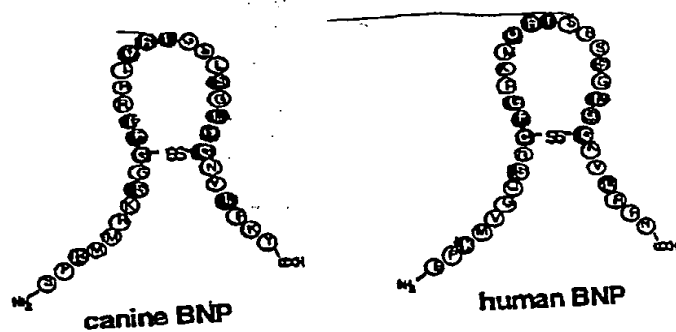


Fig 2

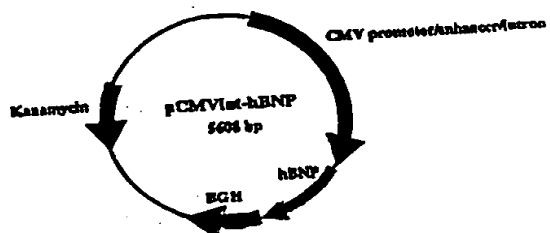


Fig 3

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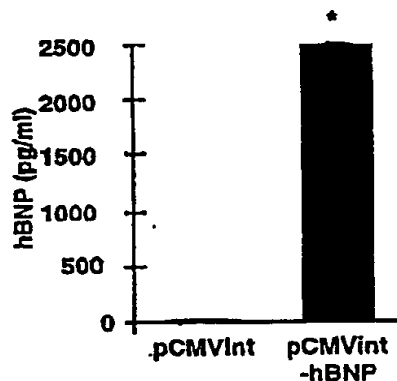


Fig 4

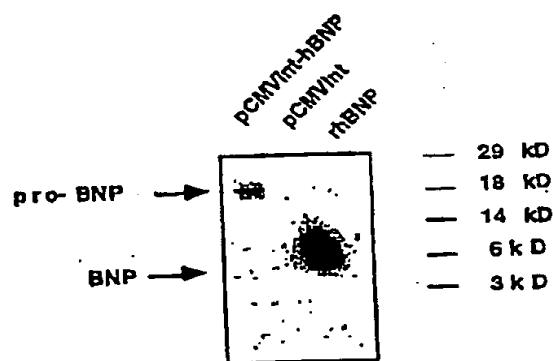


Fig 5

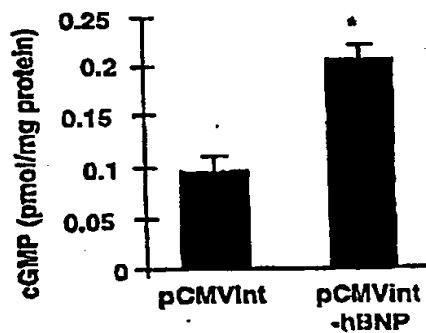


Fig 6

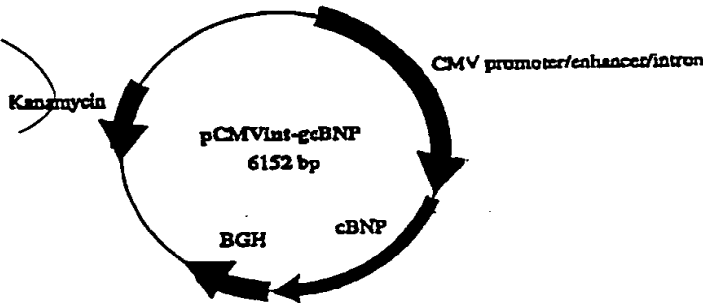


Fig 7

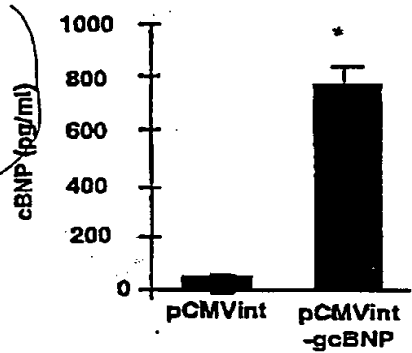


Fig 8

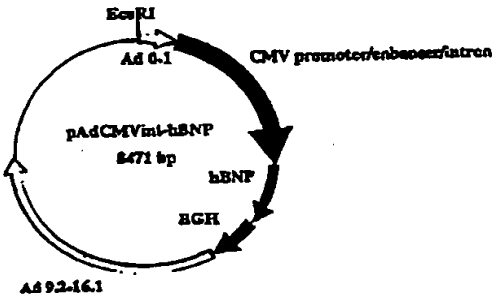


Fig 9

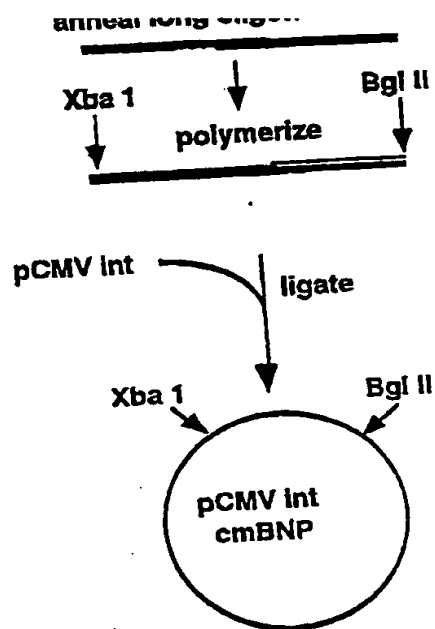


Fig 10

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Figure 11

<u>Amino Acid</u>	<u>Codon</u>
Phe	UUU, UUC
Ser	UCU, UCC, UCA, UCG, AGU, AGC
Tyr	UAU, UAC
Cys	UGU, UGC
Leu	UUA, UUG, CUU, CUC, CUA, CUG
Trp	UGG
Pro	CCU, CCC, CCA, CCG
His	CAU, CAC
Arg	CGU, CGC, CGA, CGG, AGA, AGG
Gln	CAA, CAG
Ile	AUU, AUC, AUA
Thr	ACU, ACC, ACA, ACG
Asn	AAU, AAC
Lys	AAA, AAG
Met	AUG
Val	GUU, GUC, GUA, GUG
Ala	GCU, GCC, GCA, GCG
Asp	GAU, GAC
Gly	GGU, GGC, GGA, GGG
Glu	GAA, GAG

Publ. No. 5008660

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro	pro
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala	leu
Pro (P)	gly	gly
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

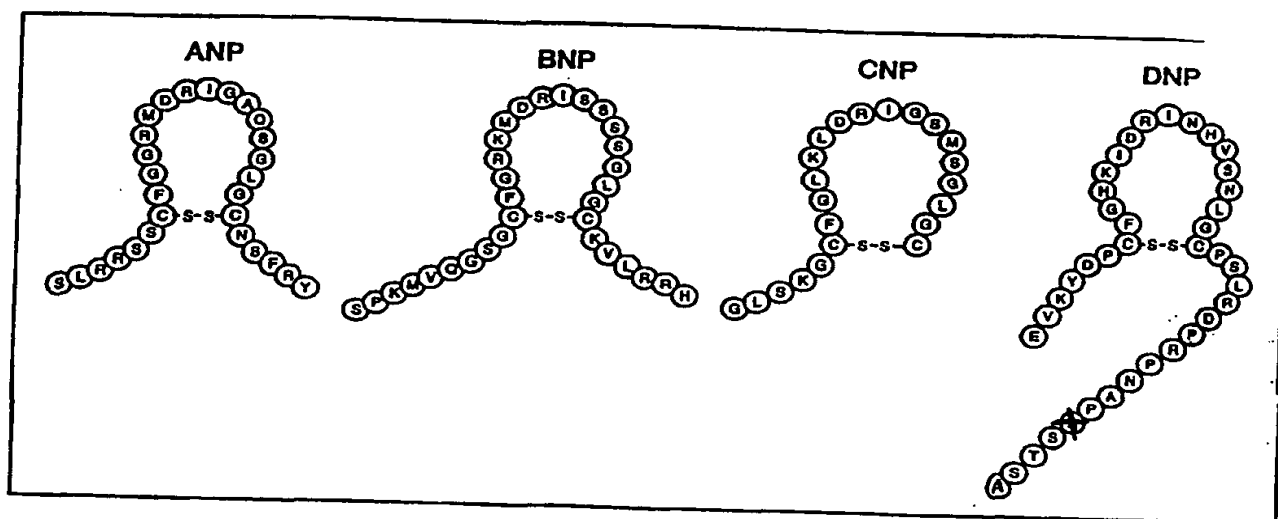


Fig. 13

A)

MDPQTAPSRALLLLFLHLAFLGGRSHPLGSPGSASDLETSGLO
EQRNHLQGLSELOVEQTSLEPLQESPRPTGVWKSREVATEGIRGHRKMVLYTLRAPR
SPKMVGSGCGFRKMDRISSSSGLGCKVLRH

B)

1	ctgtgagatc	accccggtgt	cccagcgctc	acgtcggttc	tcggaagacc	gggggtctcc
61	ctgccttttc	cagcaacggt	gggggtggga	ggcaggaaga	aagcgccaac	ctaggacccc
121	ggagattttg	agcaaaggaa	gaagcgggag	acggggcactt	gtctgtgtct	ccagcgcgtt
181	ctcgcccccc	gccgaccggg	cccatttcta	tacaaggctcg	ctctgcccg	tctccacctc
241	ccacgtgcag	gccgcgggag	ggctcattcc	cgggcctctga	tctcagagcg	ccggaattgtg
301	gctgataaat	cagagactag	agctgcattg	caggcaggcc	cgacactcag	ctccagggat
361	aaaggccacg	gtgtccccgag	gagccaggag	gagcaccctcg	cagggtgagg	gcagggtggga
421	agcaaaccgg	gacgcacatcg	agcagcagca	gcagcagcag	aagcagcagc	agcagcctcc
481	gcagctcttc	cagagacatg	gatccccaga	cagcaccttc	cctgggcgtc	ctgctcttcg
541	tcttcttgca	cttggttttc	ctgggaggtc	gttcccaacc	ctgtgggcagc	cccggttcag
601	cctcggactt	ggaaacgtcc	gggttacagg	tgagagcggg	gggcagctca	ggggggattgg
661	acagcagcaa	tgaaagggtc	ctcacctgct	gtcccaagag	gccctcatct	ttcttttgga
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901	aggtggagca	gacatccctg	gagccccctc	aggagagccc	cctgccaca	ggtgtctgga
961	agtcccggga	ggtagccacc	gagggcatcc	gtgggcaccg	caaatggtc	ctctacacc
1021	tgcgggcacc	acgaagcccc	aagatggtgc	aagggtctgg	ctgctttggg	aggaagattgg
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1201	ggaaccacac	tctttgagaa	aaggtcacct	ggacatcgct	tctcttgtt	aacagccttc
1261	agggccaag	ggtgcctttg	tggaattagt	aatgtgggc	ttatttcatt	accatgccca
1321	caataccttc	tccccacctc	ctacttctta	tcaaaggggc	agaatctctt	ttgggggtct
1381	gtttatcatt	tggcgacccc	ccagtgggtc	agaaagagaa	ccaaaccttt	cctcttggtt
1441	tctctaaac	tgtctatagt	ctcaaaggca	gagagcagga	tcaccagagc	attgataatc
1501	cccaattttac	agatgaggaa	actgaggctc	agagagttgc	attaagcctc	aaacgtctga
1561	tgactaacag	ggtgggtgggt	ggcacacgat	gaggttaagct	cagcccctgc	ctccatctcc
1621	caccttaacc	atcatacccc	tctctctttc	cctgacagtg	ctgaggcggc	attaagagga
1681	agtcctggct	gcagacacct	gcttctgatt	ccacaagggg	ctttttcttc	aacctgtggg
1741	ccgcctttga	agtgactcat	tttttttaat	gtatttatgt	atttatttga	ttgttttata
1801	taagatgggt	tcttaccttt	gagcacaata	tttcacgggt	gaaataaagt	caacattata
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1921	aa					